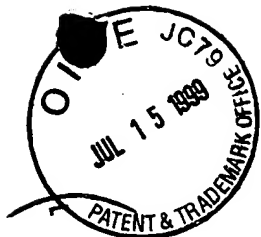


SEQUENCE LISTING



#8/c

(1) GENERAL INFORMATION:

- (i) APPLICANT: GOTO, Masaaki
TSUDA, Eisuke
MOCHIZUKI, Shin'ichi
YANO, Kazuki
KOBAYASHI, Fumie
SHIMA, Nobuyuki
YASUDA, Hisataka
NAKAGAWA, Nobuaki
MORINAGA, Tomonori
UEDA, Masatsugu
HIGASHIO, Kanji
- (ii) TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins
- (iii) NUMBER OF SEQUENCES: 108
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Testa, Hurwitz & Thibault
 - (B) STREET: 125 High St.
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/062,113
 - (B) FILING DATE: 17-APR-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 54977/1995
 - (B) FILING DATE: 20-FEB-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 207508/1995
 - (B) FILING DATE: 21-JUL-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/JP96/00374
 - (B) FILING DATE: 20-FEB-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/915,004
 - (B) FILING DATE: 20-FEB-1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: MOORE, Ronda P.
- (B) REGISTRATION NUMBER: 44,244
- (C) REFERENCE/DOCKET NUMBER: FJN-060DV

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617) 248-7000
- (B) TELEFAX: (617) 248-7100

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa Tyr His Phe Pro Lys
1 5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..14
- (D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Gln His Ser Xaa Gln Glu Gln Thr Phe Gln Leu Xaa Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..12
- (D) OTHER INFORMATION: /note= "(an internal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Xaa Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: /note= "(OCIF protein without signal peptide)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His
1 5 10 15

Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His
20 25 30

Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr
35 40 45

Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro
50 55 60

Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His
65 70 75 80

Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	85	90	95	
Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	100	105	110	
Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	115	120	125	
Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	130	135	140	
Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	145	150	155	160
Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	165	170	175	
Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	180	185	190	
Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly	195	200	205	
Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	210	215	220	
Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	225	230	235	240
Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	245	250	255	
Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	260	265	270	
Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	275	280	285	
Glu	Asp	Ile	Glu	Lys	Thr	Ile	Lys	Ala	Cys	Lys	Pro	Ser	Asp	Gln	Ile	290	295	300	
Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	305	310	315	320
Leu	Lys	Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	325	330	335	
Pro	Lys	Thr	Val	Thr	Gln	Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	340	345	350	
Ser	Phe	Thr	Met	Tyr	Lys	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	355	360	365	
Gly	Asn	Gln	Val	Gln	Ser	Val	Lys	Ile	Ser	Cys	Leu					370	375	380	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: /note= "(OCIF protein)"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0
- (D) OTHER INFORMATION: /note= "(signal peptide)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	
-20					-15					-10						
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
-5				1				5					10			
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15					20					25			
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	
		30					35					40				
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
	45					50					55					
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	
60					65				70					75		
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	
				80				85						90		
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	
			95					100					105			
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	
			110				115					120				
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	
	125					130					135					
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	
140					145					150					155	

Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	160	165	170
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	175	180	185
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	190	195	200
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	205	210	215
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	220	225	230
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	240	245	250
Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	255	260	265
Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	270	275	280
Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys	Thr	Ile	Lys	Ala	Cys	Lys	285	290	295
Pro	Ser	Asp	Gln	Ile	Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	300	305	310
Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser	320	325	330
Lys	Thr	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr	Gln	Ser	Leu	Lys	Lys	Thr	335	340	345
Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr	Lys	Leu	Tyr	Gln	Lys	Leu	350	355	360
Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	Val	Gln	Ser	Val	Lys	Ile	Ser	Cys	365	370	375
Leu																380		

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1206
(D) OTHER INFORMATION: /note= "(OCIF)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAAG	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCTTACAA	AGTTTACGCC	TAAGTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG	GCCTAATGCA	CGCACTAAAG	CACTCAAAGA	CGTACCACTT	TCCCAAAACT	1080
GTCCTCAGA	GTCTAAAGAA	GACCATCAGG	TTCCTTCACA	GCTTCACAAT	GTACAAATTG	1140
TATCAGAAGT	TATTTTGTAG	AATGATAGGT	AACCAGGTCC	AATCAGTAAA	AATAAGCTGC	1200
TTATAA						1206

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: 1..15
(D) OTHER INFORMATION: /note= "(a N-terminal amino acid sequence of the protein)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	Glu	Glu	Thr	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1185
(D) OTHER INFORMATION: /note= "(OCIF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGTGC	AATCGCACCC	ACAACCGCGT	GTGCGAATGC	300
AAGGAAGGGC	GCTACCTTGA	GATAGAGTTC	TGCTTGAAAC	ATAGGAGCTG	CCCTCCTGGA	360
TTTGGAGTGG	TGCAAGCTGG	AACCCAGAG	CGAAATACAG	TTTGCAAAAG	ATGTCCAGAT	420
GGGTCTTCT	CAAATGAGAC	GTCATCTAAA	GCACCCTGTA	GAAAACACAC	AAATTGCAGT	480
GTCTTTGGTC	TCCTGCTAAC	TCAGAAAGGA	AATGCAACAC	ACGACAACAT	ATGTTCCGGA	540
AACAGTGAAT	CAACTCAAAA	ATGTGGAATA	GATGTTACCC	TGTGTGAGGA	GGCATTCTTC	600
AGGTTTGCTG	TTCCTACAAA	GTTTACGCCT	AACGGGCTTA	GTGTCTTGGT	AGACAATTTG	660
CCTGGCACCA	AAGTAAACGC	AGAGAGTGTA	GAGAGGATAA	AACGGCAACA	CAGCTCACAA	720

GAACAGACTT TCCAGCTGCT GAAGTTATGG AAACATCAAA ACAAAGACCA AGATATAGTC 780
AAGAAGATCA TCCAAGATAT TGACCTCTGT GAAAACAGCG TGCAGCGGCA CATTGGACAT 840
GCTAACCTCA CCTTCGAGCA GCTTCGTAGC TTGATGGAAA GCTTACCGGG AAAGAAAGTG 900
GGAGCAGAAG ACATTGAAAA AACAAATAAG GCATGCAAAC CCAGTGACCA GATCCTGAAG 960
CTGCTCAGTT TGTGGCGAAT AAAAAATGGC GACCAAGACA CCTTGAAGGG CCTAATGCAC 1020
GCACTAAAGC ACTCAAAGAC GTACCACTTT CCCAAACTG TCACTCAGAG TCTAAAGAAG 1080
ACCATCAGGT TCCTTCACAG CTTCAATG TACAAATTGT ATCAGAAGTT ATTTTATAGAA 1140
ATGATAGGTA ACCAGGTCCA ATCAGTAAAA ATAAGCTGCT TATAA 1185

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..373
- (D) OTHER INFORMATION: /note= "(OCIF2)"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
30 35 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Cys Asn Arg Thr His Asn Arg
60 65 70 75

Val	Cys	Glu	Cys	Lys 80	Glu	Gly	Arg	Tyr	Leu 85	Glu	Ile	Glu	Phe	Cys	Leu
Lys	His	Arg	Ser 95	Cys	Pro	Pro	Gly	Phe 100	Gly	Val	Val	Gln	Ala 105	Gly	Thr
Pro	Glu	Arg	Asn 110	Thr	Val	Cys	Lys 115	Arg	Cys	Pro	Asp	Gly 120	Phe	Phe	Ser
Asn	Glu	Thr	Ser	Ser	Lys	Ala 130	Pro	Cys	Arg	Lys	His 135	Thr	Asn	Cys	Ser
Val 140	Phe	Gly	Leu	Leu 145	Leu	Thr	Gln	Lys	Gly	Asn 150	Ala	Thr	His	Asp	Asn 155
Ile	Cys	Ser	Gly	Asn 160	Ser	Glu	Ser	Thr	Gln 165	Lys	Cys	Gly	Ile	Asp 170	Val
Thr	Leu	Cys	Glu 175	Glu	Ala	Phe	Phe	Arg 180	Phe	Ala	Val	Pro	Thr 185	Lys	Phe
Thr	Pro	Asn 190	Trp	Leu	Ser	Val	Leu 195	Val	Asp	Asn	Leu	Pro 200	Gly	Thr	Lys
Val 205	Asn	Ala	Glu	Ser	Val	Glu 210	Arg	Ile	Lys	Arg	Gln 215	His	Ser	Ser	Gln
Glu 220	Gln	Thr	Phe	Gln 225	Leu	Leu	Lys	Leu	Trp	Lys 230	His	Gln	Asn	Lys	Asp 235
Gln	Asp	Ile	Val	Lys 240	Lys	Ile	Ile	Gln	Asp 245	Ile	Asp	Leu	Cys	Glu 250	Asn
Ser	Val	Gln	Arg 255	His	Ile	Gly	His	Ala 260	Asn	Leu	Thr	Phe	Glu 265	Gln	Leu
Arg	Ser	Leu	Met 270	Glu	Ser	Leu	Pro 275	Gly	Lys	Lys	Val	Gly 280	Ala	Glu	Asp
Ile 285	Glu	Lys	Thr	Ile	Lys	Ala 290	Cys	Lys	Pro	Ser	Asp 295	Gln	Ile	Leu	Lys
Leu 300	Leu	Ser	Leu	Trp 305	Arg	Ile	Lys	Asn	Gly	Asp 310	Gln	Asp	Thr	Leu	Lys 315
Gly	Leu	Met	His 320	Ala	Leu	Lys	His	Ser	Lys 325	Thr	Tyr	His	Phe	Pro 330	Lys
Thr	Val	Thr	Gln 335	Ser	Leu	Lys	Lys	Thr 340	Ile	Arg	Phe	Leu	His 345	Ser	Phe
Thr	Met	Tyr 350	Lys	Leu	Tyr	Gln	Lys 355	Leu	Phe	Leu	Glu	Met 360	Ile	Gly	Asn
Gln 365	Val	Gln	Ser	Val	Lys	Ile 370	Ser	Cys	Leu						

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1089
- (D) OTHER INFORMATION: /note= "(OCIF3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAACAAGT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC AGTTTGTGGC GAATAAAAAA TGGCGACCAA	900
GACACCTTGA AGGGCCTAAT GCACGCACTA AAGCACTCAA AGACGTACCA CTTTCCCAAA	960
ACTGTCACCTC AGAGTCTAAA GAAGACCATC AGGTTTCCTC ACAGCTTCAC AATGTACAAA	1020
TTGTATCAGA AGTTATTTTT AGAAATGATA GGTAACCAGG TCCAATCAGT AAAAATAAGC	1080
TGCTTATAA	1089

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..341
 (D) OTHER INFORMATION: /note= "(OCIF3)"

- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Asn	Lys	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	
-20						-15					-10					
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
-5				1				5						10		
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15					20					25			
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	
		30					35					40				
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
	45					50					55					
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	
60					65				70					75		
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	
			80					85						90		
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	
			95					100					105			
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	
			110				115					120				
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	
	125					130					135					
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	
140					145					150					155	

Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	160	165	170
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	175	180	185
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	190	195	200
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	205	210	215
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	220	225	230
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	240	245	250
Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	255	260	265
Asn	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	270	275	280
Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	Lys	285	290	295
Thr	Val	Thr	Gln	Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	Ser	Phe	300	305	310
Thr	Met	Tyr	Lys	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn	320	325	330
Gln	Val	Gln	Ser	Val	Lys	Ile	Ser	Cys	Leu							335	340	

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..465
- (D) OTHER INFORMATION: /note= "(OCIF4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGAACAAGT TGCTGTGCTG CTCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC

CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG 120
 TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC 180
 GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT 240
 CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC 300
 CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA 360
 CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GTACGTGTCA ATGTGCAGCA 420
 AAATTAATTA GGATCATGCA AAGTCAGATA GTTGTGACAG TTTAG 465

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..133
- (D) OTHER INFORMATION: /note= "(OCIF4)"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Asn	Lys	Leu	Leu	Cys	Cys	Ser	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	
	-20					-15					-10					
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
-5				1				5					10			
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15					20					25			
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	
		30					35					40				
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
		45				50					55					
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	
60					65				70					75		
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	
				80					85					90		

Ile Met Gln Ser Gln Ile Val Val Thr Val
125 130

(ix) FEATURE:

(A) NAME/KEY: Protein
(B) LOCATION: 1..124
(D) OTHER INFORMATION: /note= "(OCIF5)"

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: -21..0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Asn	Lys	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	
-20					-15					-10						
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
-5				1				5					10			
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15					20					25			
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	
	30						35					40				
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
45						50					55					
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	
60					65					70					75	
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	
				80					85					90		
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	
			95					100					105			
Gly	Val	Val	Gln	Ala	Gly	Cys	Arg	Arg	Arg	Pro	Lys	Pro	Gln	Ile	Cys	
	110						115					120				

Ile

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "synthetic DNA (primer T3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATTAACCCT CACTAAAGGG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..22
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer T7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAATACGAC TCACTATAGG GC

22

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACATCAAAAC AAAGACCAAG

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20

(D) OTHER INFORMATION: /note= "synthetic DNA (primer IF2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCTTGGTCTT TGTTTTGATG

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTATTCGCCA CAAACTGAGC

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTGTGAAGCT GTGAAGGAAC

20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF5)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCTCAGTTTG TGGCGAATAA

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF6)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGGGAGCAG AAGACATTGA

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF7)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AATGAACAAC TTGCTGTGCT

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF8)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGACAAATGT CCTCCTGGTA

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF9)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGGTAGGTAC CAGGAGGACA

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF10)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAGCTGCCCT CCTGGATTG

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF11)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAAACGTAT TTCGCTCTGG

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer IF12)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGTGAGGAG GCATTCTTCA

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer C19SF)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAATCAACTC AAAAAAGTGG AATAGATGTT AC

32

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer C19SR)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTAACATCTA TTCCACTTTT TTGAGTTGAT TC

32

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer C20SF)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATAGATGTTA CCCTGAGTGA GGAGGCATTC

30

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
C20SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAATGCCTCC TCACTCAGGG TAACATCTAT

30

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..31
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
C21SF) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAAGATATTG ACCTCAGTGA AAACAGCGTG C

31

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..31
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
C21SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCACGCTGTT TTCCTGAGG GCAATATCTT G

31

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..31
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
C22SF)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAAACAATAA AGGCAAGCAA ACCCAGTGAC C

31

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..31
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
C22SR)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGTCACTGGG TTTGCTTGCC TTTATTGTTT T

31

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..31
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
C23SF)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCAGTAAAAA TAAGCAGCTT ATAAGTGGCC A

31

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..31
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer
C23SR) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TGGCCAGTTA TAAGCTGCTT ATTTTACTG A

31

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..22
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer
IF14) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTGGGGTTTA TTGGAGGAGA TG

22

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..36
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR1F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCACCCAGG AACCTTGCCC TGACCACTAC TACACA

36

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR1R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTCAGGGCAA GGTTCCCTGGG TGGTCCACTT AATGGA

36

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR2F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACCGTGTGCG CCGAATGCAA GGAAGGGCGC TACCTT

36

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..36
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR2R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:
TTCCTTGCAT TCGGCGCACA CGGTCTTCCA CTTTGC 36

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..36
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR3F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
AACCGCGTGT GCAGATGTCC AGATGGGTTC TTCTCA 36

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..36
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer
DCR3R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
ATCTGGACAT CTGCACACGC GGTTGTGGGT GCGATT 36

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR4F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAGTTTGCA AATCCGGAAA CAGTGAATCA ACTCAA

36

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DCR4R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTGTTTCCG GATTTGCAAA CTGTATTTCG CTCTGG

36

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DDD1F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AATGTGGAAT AGATATTGAC CTCTGTGAAA ACAGCG

36

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DDD1R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGAGGTCAAT ATCTATTCCA CATTTTGTAG TTGATT

36

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer DDD2F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGATCATCCA AGACGCACTA AAGCACTCAA AGACGT

36

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..36
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
DDD2R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCTTTAGTGC GTCTTGATG ATCTTCTTGA CTATAT

36

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..29
(D) OTHER INFORMATION: /note= "synthetic DNA (primer XhoI
F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGCTCGAGCG CCCAGCCGCC GCCTCCAAG

29

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "synthetic DNA (primer
IF16) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTTGAGTGCT TTAGTGCGTG

20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CL
F) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TCAGTAAAAA TAAGCTAACT GGAAATGGCC

30

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CL
R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCCATTTCC AGTTAGCTTA TTTTACTGA

30

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..29
(D) OTHER INFORMATION: /note= "synthetic DNA (primer CC
R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCGGATCCTC AGTGCTTTAG TGC GTGCAT

29

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..29
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer CCD2
R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCGGATCCTC ATTGGATGAT CTTCTTGAC

29

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..29
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer CCD1
R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCGGATCCTC ATATTCCACA TTTTGTGAGT

29

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..29
 (D) OTHER INFORMATION: /note= "synthetic DNA (primer CCR4
R) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCGGATCCTC ATTTGCAAAC TGTATTTTCG

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..29
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer CCR3 R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCGGATCCTC ATTCGCACAC GCGGTTGTG

29

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: /note= "OCIF-C19S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr

15					20					25					
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro
		30					35					40			
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys
	45					50					55				
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu
60					65					70					75
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr
				80					85					90	
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe
			95					100					105		
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg
		110					115					120			
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys
	125					130					135				
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys
140					145					150					155
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr
				160					165					170	
Gln	Lys	Ser	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg
			175					180					185		
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val
		190					195					200			
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile
	205					210					215				
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu
220					225					230					235
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln
				240					245					250	
Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala
			255					260					265		
Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly
		270					275					280			
Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys	Thr	Ile	Lys	Ala	Cys	Lys
	285					290					295				
Pro	Ser	Asp	Gln	Ile	Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn
300					305					310					315
Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser

				320						325						330			
Lys	Thr	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr	Gln	Ser	Leu	Lys	Lys	Thr				
			335					340					345						
Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr	Lys	Leu	Tyr	Gln	Lys	Leu				
		350					355					360							
Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	Val	Gln	Ser	Val	Lys	Ile	Ser	Cys				
	365					370					375								
Leu																			
380																			

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: /note= "OCIF-C20S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile				
-20					-15					-10									
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp				
-5				1				5					10						
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr				
			15					20					25						
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro				
	30						35					40							
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys				
	45					50					55								
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu				
60					65				70						75				
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr				
			80						85					90					

[illegible]

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 401 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: -21..0

- (ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..380
 (D) OTHER INFORMATION: /note= "OCIF-C21S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	
-20					-15					-10						
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
-5				1				5						10		
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15					20						25		
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	
		30					35					40				
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
	45					50					55					
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	
60					65				70						75	
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	
				80					85						90	
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	
			95					100						105		
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	
			110				115					120				
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	
	125					130					135					
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	
140					145					150					155	

Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	160	165	170
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	175	180	185
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	190	195	200
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	205	210	215
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	220	225	230
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	240	245	250
Asp	Ile	Asp	Leu	Ser	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	255	260	265
Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	270	275	280
Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys	Thr	Ile	Lys	Ala	Cys	Lys	285	290	295
Pro	Ser	Asp	Gln	Ile	Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	300	305	310
Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser	320	325	330
Lys	Thr	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr	Gln	Ser	Leu	Lys	Lys	Thr	335	340	345
Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr	Lys	Leu	Tyr	Gln	Lys	Leu	350	355	360
Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	Val	Gln	Ser	Val	Lys	Ile	Ser	Cys	365	370	375
Leu																380		

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: -21..0

(ix) FEATURE:

(A) NAME/KEY: Protein
(B) LOCATION: 1..380
(D) OTHER INFORMATION: /note= "OCIF-C22S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	
	-20					-15					-10					
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
-5				1				5					10			
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15					20					25			
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	
	30						35					40				
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
	45					50					55					
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	
60					65				70					75		
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	
			80					85						90		
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	
			95					100					105			
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	
	110						115					120				
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	
	125					130					135					
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	
140					145					150					155	
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	
				160					165					170		
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	
			175					180					185			
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	
	190						195					200				
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	
	205					210					215					
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	

220		225		230		235									
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln
				240					245					250	
Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala
			255					260					265		
Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly
		270					275					280			
Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys	Thr	Ile	Lys	Ala	Ser	Lys
	285					290					295				
Pro	Ser	Asp	Gln	Ile	Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn
300					305					310					315
Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser
				320					325					330	
Lys	Thr	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr	Gln	Ser	Leu	Lys	Lys	Thr
			335					340					345		
Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr	Lys	Leu	Tyr	Gln	Lys	Leu
		350					355					360			
Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	Val	Gln	Ser	Val	Lys	Ile	Ser	Cys
	365					370					375				
Leu															
380															

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: /note= "OCIF-C23S"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
-20						-15					-10				

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 5 10
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
 30 35 40
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 45 50 55
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
 60 65 70 75
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
 80 85 90
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
 95 100 105
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
 110 115 120
 Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
 125 130 135
 Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
 140 145 150 155
 Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
 160 165 170
 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
 175 180 185
 Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
 190 195 200
 Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 205 210 215
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 220 225 230 235
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln
 240 245 250
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
 255 260 265
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
 270 275 280
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
 285 290 295

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 300 305 310 315
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
 320 325 330
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
 335 340 345
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
 350 355 360
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Ser
 365 370 375
 Leu
 380

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0

- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..339
 - (D) OTHER INFORMATION: /note= "OCIF-DCR1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
 Lys Trp Thr Thr Gln Glu Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser
 -5 1 5 10
 Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu
 15 20 25
 Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
 30 35 40
 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys His
 45 50 55

Arg	Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	60	65	70	75
Arg	Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	80	85	90	
Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	95	100	105	
Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	110	115	120	
Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	125	130	135	
Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	140	145	150	155
Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	160	165	170	
Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	175	180	185	
Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	190	195	200	
Ile	Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	205	210	215	
Gln	Arg	His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	220	225	230	235
Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	240	245	250	
Lys	Thr	Ile	Lys	Ala	Cys	Lys	Pro	Ser	Asp	Gln	Ile	Leu	Lys	Leu	Leu	255	260	265	
Ser	Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	270	275	280	
Met	His	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	Lys	Thr	Val	285	290	295	
Thr	Gln	Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	300	305	310	315
Tyr	Lys	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	Val	320	325	330	
Gln	Ser	Val	Lys	Ile	Ser	Cys	Leu									335			

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: -21..0

(ix) FEATURE:

(A) NAME/KEY: Protein
(B) LOCATION: 1..338
(D) OTHER INFORMATION: /note= "OCIF-DCR2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	
-20					-15					-10						
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
-5				1				5						10		
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15					20						25		
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Glu	
	30						35					40				
Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	
45						50				55						
Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	
60					65					70					75	
Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	
			80						85					90		
Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	
			95					100						105		
Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	
			110				115						120			
Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	
	125					130					135					
Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	
140					145					150					155	
Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	
			160					165						170		
Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	

	175		180		185										
Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile
	190						195					200			
Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln
	205					210					215				
Arg	His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu
220					225					230					235
Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys
				240					245					250	
Thr	Ile	Lys	Ala	Cys	Lys	Pro	Ser	Asp	Gln	Ile	Leu	Lys	Leu	Leu	Ser
			255					260					265		
Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met
	270						275						280		
His	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr
	285					290					295				
Gln	Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr
300					305					310					315
Lys	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	Val	Gln
				320					325					330	
Ser	Val	Lys	Ile	Ser	Cys	Leu									
						335									

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: /note= "OCIF-DCR3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
-20						-15					-10				

Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
-5					1				5					10		
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15					20					25			
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	
		30					35					40				
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
	45					50					55					
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	
60					65					70					75	
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	
				80					85					90		
Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	Cys	
			95					100						105		
Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	
		110					115					120				
Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	
	125					130					135					
Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	
140					145					150					155	
Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly	Thr	
				160					165					170		
Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	Ser	
		175						180					185			
Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	Lys	
		190					195					200				
Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	
	205					210					215					
Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	Gln	
220					225					230					235	
Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	Glu	
				240					245					250		
Asp	Ile	Glu	Lys	Thr	Ile	Lys	Ala	Cys	Lys	Pro	Ser	Asp	Gln	Ile	Leu	
		255						260					265			
Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	
		270					275					280				
Lys	Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	
	285					290					295					

Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser
 300 305 310 315
 Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly
 320 325 330
 Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu
 335 340

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: -21..0

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..338
 (D) OTHER INFORMATION: /note= "OCIF-DCR4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 5 10
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
 30 35 40
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 45 50 55
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
 60 65 70 75
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
 80 85 90
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
 95 100 105

Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Ser	110	115	120
Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	125	130	135
Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	140	145	150
Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	160	165	170
Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	175	180	185
Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	190	195	200
Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	205	210	215
Arg	His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	220	225	230
Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys	240	245	250
Thr	Ile	Lys	Ala	Cys	Lys	Pro	Ser	Asp	Gln	Ile	Leu	Lys	Leu	Leu	Ser	255	260	265
Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	270	275	280
His	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr	285	290	295
Gln	Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr	300	305	310
Lys	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	Val	Gln	320	325	330
Ser	Val	Lys	Ile	Ser	Cys	Leu										335		

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Peptide
(B) LOCATION: -21..0

(ix) FEATURE:

(A) NAME/KEY: Protein
(B) LOCATION: 1..305
(D) OTHER INFORMATION: /note= "OCIF-DDD1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	
-20					-15						-10					
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
-5				1				5					10			
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15					20					25			
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	
	30						35					40				
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
45						50					55					
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	
60					65					70					75	
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	
				80					85					90		
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	
			95					100						105		
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	
			110				115						120			
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	
	125					130					135					
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	
140					145					150					155	
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	
				160					165					170		
Gln	Lys	Cys	Gly	Ile	Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	
			175					180					185			
His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	Met	
		190					195					200				
Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys	Thr	
	205					210					215					
Ile	Lys	Ala	Cys	Lys	Pro	Ser	Asp	Gln	Ile	Leu	Lys	Leu	Leu	Ser	Leu	

220		225		230		235									
Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	His
				240					245					250	
Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr	Gln
			255					260					265		
Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr	Lys
			270				275					280			
Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	Val	Gln	Ser
	285					290					295				
Val	Lys	Ile	Ser	Cys	Leu										
300					305										

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..306
- (D) OTHER INFORMATION: /note= "OCIF-DDD2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
-20					-15					-10					
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp
-5				1					5					10	
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr
			15					20					25		
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro
	30						35					40			
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys
45						50					55				
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu
60					65					70					75

Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	
				80					85					90		
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	
			95					100						105		
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	
			110				115					120				
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	
	125						130					135				
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	
140					145					150					155	
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	
				160					165						170	
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	
			175					180						185		
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	
		190					195					200				
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	
	205						210					215				
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	
220					225					230					235	
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	
				240					245					250		
Asp	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr	
			255					260						265		
Gln	Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr	
		270					275					280				
Lys	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	Val	Gln	
	285					290					295					
Ser	Val	Lys	Ile	Ser	Cys	Leu										
300					305											

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: -21..0

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..378

(D) OTHER INFORMATION: /note= "OCIF-CL"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	
	-20					-15					-10					
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	
-5				1				5					10			
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	
			15					20					25			
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	
	30						35					40				
Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys	
45						50					55					
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu	
60					65				70					75		
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr	
				80					85					90		
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe	
			95					100					105			
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg	
	110						115					120				
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	
	125					130					135					
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	
140					145					150					155	
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	
				160					165					170		
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	
			175					180					185			
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	
	190						195					200				
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	
205						210					215					

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 220 225 230 235
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln
 240 245 250
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
 255 260 265
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
 270 275 280
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys
 285 290 295
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn
 300 305 310 315
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser
 320 325 330
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr
 335 340 345
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu
 350 355 360
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser
 365 370 375

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: /note= "OCIF-CC"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp

-5	1	5	10
Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr	15	20	25
Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro	30	35	40
Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys	45	50	55
Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu	60	65	70
Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr	80	85	90
Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe	95	100	105
Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg	110	115	120
Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys	125	130	135
Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys	140	145	150
Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr	160	165	170
Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg	175	180	185
Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val	190	195	200
Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile	205	210	215
Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu	220	225	230
Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln	240	245	250
Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala	255	260	265
Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly	270	275	280
Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys	285	290	295
Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn			

Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	140	145	150	155
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	160	165	170	
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	175	180	185	
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	190	195	200	
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	205	210	215	
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	220	225	230	235
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	240	245	250	

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: /note= "OCIF-CDD1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile	-20	-15	-10	
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	-5	1	5	10
Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	Lys	Cys	Pro	Pro	Gly	Thr	15	20	25	
Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	Lys	Thr	Val	Cys	Ala	Pro	30	35	40	

Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	His	Thr	Ser	Asp	Glu	Cys
45						50					55				
Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	Gln	Tyr	Val	Lys	Gln	Glu
60					65					70					75
Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	Cys	Lys	Glu	Gly	Arg	Tyr
			80						85					90	
Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	Ser	Cys	Pro	Pro	Gly	Phe
			95					100					105		
Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	Asn	Thr	Val	Cys	Lys	Arg
		110					115					120			
Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys
		125				130					135				
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys
140					145					150					155
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr
				160					165					170	
Gln	Lys	Cys	Gly	Ile											
			175												

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0

- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: /note= "OCIF-CCR4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met	Asn	Asn	Leu	Leu	Cys	Cys	Ala	Leu	Val	Phe	Leu	Asp	Ile	Ser	Ile
-20						-15					-10				
Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp
-5				1				5						10	

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
 30 35 40
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 45 50 55
 Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
 60 65 70 75
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
 80 85 90
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
 95 100 105
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys
 110 115 120

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: /note= "OCIF-CCR3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 5 10
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
 30 35 40
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys

45	50	55
Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu		
60	65	70 75
Cys Asn Arg Thr His Asn Arg Val Cys Glu		
	80	85

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: -21..0

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..372
- (D) OTHER INFORMATION: /note= "OCIF-CBst"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile		
-20	-15	-10
Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp		
-5	1	5 10
Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr		
	15	20 25
Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro		
	30	35 40
Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys		
	45	50 55
Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu		
60	65	70 75
Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr		
	80	85 90
Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe		
	95	100 105
Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg		
	110	115 120

Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	Ser	Ser	Lys	Ala	Pro	Cys	125	130	135
Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	Leu	Leu	Leu	Thr	Gln	Lys	140	145	150
Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	Gly	Asn	Ser	Glu	Ser	Thr	160	165	170
Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	175	180	185
Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	190	195	200
Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	205	210	215
Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	220	225	230
Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	Val	Lys	Lys	Ile	Ile	Gln	240	245	250
Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln	Arg	His	Ile	Gly	His	Ala	255	260	265
Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu	Met	Glu	Ser	Leu	Pro	Gly	270	275	280
Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys	Thr	Ile	Lys	Ala	Cys	Lys	285	290	295
Pro	Ser	Asp	Gln	Ile	Leu	Lys	Leu	Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	300	305	310
Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met	His	Ala	Leu	Lys	His	Ser	320	325	330
Lys	Thr	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr	Gln	Ser	Leu	Lys	Lys	Thr	335	340	345
Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr	Lys	Leu	Tyr	Gln	Lys	Leu	350	355	360
Phe	Leu	Glu	Met	Ile	Gly	Asn	Leu	Val								365	370	

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: -21..0

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..300

(D) OTHER INFORMATION: /note= "OCIF-CSph"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
-20 -15 -10

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
-5 1 5 10

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
15 20 25

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
30 35 40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45 50 55

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
60 65 70 75

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
80 85 90

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
95 100 105

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
110 115 120

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
125 130 135

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
140 145 150 155

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
160 165 170

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
175 180 185

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
190 195 200

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
 205 210 215
 Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu
 220 225 230 235
 Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln
 240 245 250
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala
 255 260 265
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly
 270 275 280
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Ser Leu
 285 290 295
 Asp
 300

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0

- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..166
 - (D) OTHER INFORMATION: /note= "OCIF-CBsp"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 -20 -15 -10
 Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 -5 1 5 10
 Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 15 20 25
 Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
 30 35 40
 Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys

45		50		55
Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu				
60		65		70
Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr				
	80		85	90
Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe				
	95		100	105
Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg				
	110		115	120
Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys				
	125		130	135
Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys				
140		145		150
Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly				
	160		165	

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: -21..0

- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..63
 - (D) OTHER INFORMATION: /note= "OCIF-CPst"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Asn Asn Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile				
-20		-15		-10
Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp				
-5		1		5
				10
Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr				
	15		20	25
Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro				
	30		35	40

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
45 50 55

Leu Tyr Leu Val
60

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C19S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ATGAACA	ACT	TGCTGT	GCTG	CGCGCT	CGTG	TTTCTG	GACA	TCTCCA	TTAA	GTGGAC	CACC	60
CAGGAA	ACGT	TTCCTC	CAAA	GTACCT	TCAT	TATGAC	GAAG	AAACCT	CTCA	TCAGCT	GTTG	120
TGTGAC	AAAT	GTCCTC	CCTG	TACCTA	CCTA	AAACA	AACT	GTACAG	CAAA	GTGGA	AGACC	180
GTGTGC	GCCC	CTTGCC	CTGA	CCACTA	CTAC	ACAGAC	AGCT	GGCAC	ACCAG	TGACG	AGTGT	240
CTATA	CTGCA	GCCCCG	TGTG	CAAGG	AGCTG	CAGTAC	GTCA	AGCAG	GAGTG	CAATCG	CACC	300
CACAAC	CGCG	TGTGCG	AATG	CAAGGA	AGGG	CGCTAC	CTTG	AGATAG	AGTT	CTGCTT	GAAA	360
CATAGG	AGCT	GCCCTC	CCTG	ATTTGG	AGTG	GTGCA	AGCTG	GAACCC	CAGA	GCGAA	ATACA	420
GTTTG	CAAAA	GATGTC	CAGA	TGGGTT	CTTC	TCAAAT	GAGA	CGTCAT	CTAA	AGCAC	CCTGT	480
AGAAA	ACACA	CAAATT	GCAG	TGTCTT	TGGT	CTCCTG	CTAA	CTCAG	AAAG	AAATG	CAACA	540
CACGAC	AACA	TATGTT	CCGG	AAACAG	TGAA	TCAACT	CAAA	AAAGT	GGAAT	AGATGT	TACC	600
CTGTGT	GAGG	AGGCAT	TCTT	CAGGTT	TGCT	GTTCTT	TACAA	AGTTT	TACGC	TAAC	TGGCTT	660
AGTGT	CCTGG	TAGACA	ATTT	GCCTGG	CACC	AAAGTA	AACG	CAGAG	AGTGT	AGAG	AGGATA	720
AAACG	GCAAC	ACAGCT	CACA	AGAAC	CAGACT	TTCCAG	CTGC	TGAAG	TTATG	GAAAC	ATCAA	780
AACAA	AGACC	AAGATA	TAGT	CAAGA	AGATC	ATCCA	AGATA	TTGAC	CTCTG	TGAAA	ACAGC	840
GTGCAG	CGGC	ACATTG	GACA	TGCTAA	CCTC	ACCTTC	GAGC	AGCTTC	CGTAG	CTTGAT	GGAA	900
AGCTT	ACCGG	GAAAG	AAAGT	GGGAG	CAGAA	GACATT	GAAA	AAACA	ATAAA	GGCAT	GCAA	960

CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT	1080
GTCACTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG	1140
TATCAGAAGT TATTTT TAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC	1200
TTATAA	1206

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C20S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCA GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC	600
CTGAGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840

GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAAACT	1080
GTCCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG	1140
TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC	1200
TTATAA	1206

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C21S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720

AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCAG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT	1080
GTCACCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG	1140
TATCAGAAGT TATTTT TAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC	1200
TTATAA	1206

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C22S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ATGAACAAC TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCCTC TCAAATGAGA CGTCATCTAA AGCACCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC	600

CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCAAGCAAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT	1080
GTCCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG	1140
TATCAGAAGT TATTTT TAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTGC	1200
TTATAA	1206

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: /note= "(OCIF-C23S)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCCTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT	480

AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT	1080
GTCCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG	1140
TATCAGAAGT TATTTT TAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCAGC	1200
TTATAA	1206

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1083 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1083
 - (D) OTHER INFORMATION: /note= "(OCIF-DCR1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAACCTT GCCCTGACCA CTACTACACA GACAGCTGGC ACACCAGTGA CGAGTGTCTA	120
TACTGCAGCC CCGTGTGCAA GGAGCTGCAG TACGTCAAGC AGGAGTGCAA TCGCACCCAC	180
AACCGCGTGT GCGAATGCAA GGAAGGGCGC TACCTTGAGA TAGAGTTCTG CTTGAAACAT	240
AGGAGCTGCC CTCCTGGATT TGGAGTGGTG CAAGCTGGAA CCCCAGAGCG AAATACAGTT	300
TGCAAAAGAT GTCCAGATGG GTTCTTCTCA AATGAGACGT CATCTAAAGC ACCCTGTAGA	360

AAACACACAA ATTGCAGTGT CTTTGGTCTC CTGCTAACTC AGAAAGGAAA TGCAACACAC	420
GACAACATAT GTTCCGGAAG CAGTGAATCA ACTCAAAAAT GTGGAATAGA TGTTACCCTG	480
TGTGAGGAGG CATTCCTCAG GTTTGCTGTT CCTACAAAGT TTACGCCTAA CTGGCTTAGT	540
GTCTTGGTAG ACAATTTGCC TGGCACCAAA GTAAACGCAG AGAGTGTAGA GAGGATAAAA	600
CGGCAACACA GCTCACAAGA ACAGACTTTC CAGCTGCTGA AGTTATGGAA ACATCAAAAC	660
AAAGACCAAG ATATAGTCAA GAAGATCATC CAAGATATTG ACCTCTGTGA AAACAGCGTG	720
CAGCGGCACA TTGGACATGC TAACCTCACC TTCGAGCAGC TTCGTAGCTT GATGGAAAGC	780
TTACCGGGAA AGAAAGTGGG AGCAGAAGAC ATTGAAAAA CAATAAAGGC ATGCAAACCC	840
AGTGACCAGA TCCTGAAGCT GCTCAGTTTG TGGCGAATAA AAAATGGCGA CCAAGACACC	900
TTGAAGGGCC TAATGCACGC ACTAAAGCAC TCAAAGACGT ACCACTTTCC CAAAACCTGTC	960
ACTCAGAGTC TAAAGAAGAC CATCAGGTTT CTTACAGCT TCACAATGTA CAAATTGTAT	1020
CAGAAGTTAT TTTTAGAAAT GATAGGTAAC CAGGTCCAAT CAGTAAAAAT AAGCTGCTTA	1080
TAA	1083

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1080 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1080
 - (D) OTHER INFORMATION: /note= "(OCIF-DCR2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCG AATGCAAGGA AGGGCGCTAC CTTGAGATAG AGTTCTGCTT GAAACATAGG	240
AGCTGCCCTC CTGGATTTGG AGTGGTGCAA GCTGGAACCC CAGAGCGAAA TACAGTTTGC	300
AAAAGATGTC CAGATGGGTT CTTCTCAAAT GAGACGTCAT CTAAAGCACC CTGTAGAAAA	360

CACACAAATT GCAGTGTCTT TGGTCTCCTG CTAATCAGA AAGGAAATGC AACACACGAC	420
AACATATGTT CCGGAAACAG TGAATCAACT CAAAAATGTG GAATAGATGT TACCCTGTGT	480
GAGGAGGCAT TCTTCAGGTT TGCTGTTCCCT ACAAAGTTTA CGCCTAACTG GCTTAGTGTG	540
TTGGTAGACA ATTTGCCTGG CACCAAAGTA AACGCAGAGA GTGTAGAGAG GATAAAACGG	600
CAACACAGCT CACAAGAACA GACTTTCCAG CTGCTGAAGT TATGGAAACA TCAAAACAAA	660
GACCAAGATA TAGTCAAGAA GATCATCCAA GATATTGACC TCTGTGAAAA CAGCGTGCAG	720
CGGCACATTG GACATGCTAA CCTCACCTTC GAGCAGCTTC GTAGCTTGAT GGAAAGCTTA	780
CCGGGAAAGA AAGTGGGAGC AGAAGACATT GAAAAAACA TAAAGGCATG CAAACCCAGT	840
GACCAGATCC TGAAGCTGCT CAGTTTGTGG CGAATAAAAA ATGGCGACCA AGACACCTTG	900
AAGGGCCTAA TGCACGCACT AAAGCACTCA AAGACGTACC ACTTTCCCAA AACTGTCACT	960
CAGAGTCTAA AGAAGACCAT CAGGTCCTT CACAGCTTCA CAATGTACAA ATTGTATCAG	1020
AAGTTATTTT TAGAAATGAT AGGTAACCAG GTCCAATCAG TAAAAATAAG CTGCTTATAA	1080

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1092
- (D) OTHER INFORMATION: /note= "(OCIF-DCR3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCAGATG TCCAGATGGG TTCTTCTCAA ATGAGACGTC ATCTAAAGCA	360

CCCTGTAGAA AACACACAAA TTGCAGTGTC TTTGGTCTCC TGCTAACTCA GAAAGGAAAT	420
GCAACACACG ACAACATATG TTCCGGAAAC AGTGAATCAA CTCAAAAATG TGGGAATAGAT	480
GTTACCCTGT GTGAGGAGGC ATTCTTCAGG TTTGCTGTTC CTACAAAGTT TACGCCTAAC	540
TGGCTTAGTG TCTTGGTAGA CAATTTGCCT GGCACCAAAG TAAACGCAGA GAGTGTAGAG	600
AGGATAAAAC GGCAACACAG CTCACAAGAA CAGACTTTCC AGCTGCTGAA GTTATGGAAA	660
CATCAAAACA AAGACCAAGA TATAGTCAAG AAGATCATCC AAGATATTGA CCTCTGTGAA	720
AACAGCGTGC AGCGGCACAT TGGACATGCT AACCTCACCT TCGAGCAGCT TCGTAGCTTG	780
ATGGAAAGCT TACCGGGAAA GAAAGTGGGA GCAGAAGACA TTGAAAAAAC AATAAAGGCA	840
TGCAAACCCA GTGACCAGAT CCTGAAGCTG CTCAGTTTGT GGCGAATAAA AAATGGCGAC	900
CAAGACACCT TGAAGGGCCT AATGCACGCA CTAAAGCACT CAAAGACGTA CCACTTTCCC	960
AAAAGTGTCA CTCAGAGTCT AAAGAAGACC ATCAGGTTC TACACAGCTT CACAATGTAC	1020
AAATTGTATC AGAAGTTATT TTTAGAAATG ATAGGTAACC AGGTCCAATC AGTAAAAATA	1080
AGCTGCTTAT AA	1092

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1080
- (D) OTHER INFORMATION: /note= "(OCIF-DCR4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360

CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420
GTTTGCAAAT	CCGGAAACAG	TGAATCAACT	CAAAAATGTG	GAATAGATGT	TACCCTGTGT	480
GAGGAGGCAT	TCTTCAGGTT	TGCTGTTCCT	ACAAAGTTTA	CGCCTAACTG	GCTTAGTGTC	540
TTGGTAGACA	ATTTGCCTGG	CACCAAAGTA	AACGCAGAGA	GTGTAGAGAG	GATAAAACGG	600
CAACACAGCT	CACAAGAACA	GACTTTCAG	CTGCTGAAGT	TATGGAAACA	TCAAAACAAA	660
GACCAAGATA	TAGTCAAGAA	GATCATCCAA	GATATTGACC	TCTGTGAAAA	CAGCGTGCAG	720
CGGCACATTG	GACATGCTAA	CCTCACCTTC	GAGCAGCTTC	GTAGCTTGAT	GGAAAGCTTA	780
CCGGGAAAGA	AAGTGGGAGC	AGAAGACATT	GAAAAAACAA	TAAAGGCATG	CAAACCCAGT	840
GACCAGATCC	TGAAGCTGCT	CAGTTTGTGG	CGAATAAAAA	ATGGCGACCA	AGACACCTTG	900
AAGGGCCTAA	TGCACGCACT	AAAGCACTCA	AAGACGTACC	ACTTTCCTAA	AACTGTCACT	960
CAGAGTCTAA	AGAAGACCAT	CAGGTTTCCT	CACAGCTTCA	CAATGTACAA	ATTGTATCAG	1020
AAGTTATTTT	TAGAAATGAT	AGGTAACCAG	GTCCAATCAG	TAAAAATAAG	CTGCTTATAA	1080

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 981 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..981
 - (D) OTHER INFORMATION: /note= "(OCIF-DDD1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGAACAACT	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAGA	GCGAAATACA	420

GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATATTGAC	600
CTCTGTGAAA ACAGCGTGCA GCGGCACATT GGACATGCTA ACCTCACCTT CGAGCAGCTT	660
CGTAGCTTGA TGGAAAGCTT ACCGGGAAAG AAAGTGGGAG CAGAAGACAT TGAAAAACA	720
ATAAAGGCAT GCAAACCCAG TGACCAGATC CTGAAGCTGC TCAGTTTGTG GCGAATAAAA	780
AATGGCGACC AAGACACCTT GAAGGGCCTA ATGCACGCAC TAAAGCACTC AAAGACGTAC	840
CACTTTCCCA AAAGTGTAC TCAGAGTCTA AAGAAGACCA TCAGGTTCTT TCACAGCTTC	900
ACAATGTACA AATTGTATCA GAAGTTATTT TTAGAAATGA TAGGTAACCA GGTCCAATCA	960
GTAAAAATAA GCTGCTTATA A	981

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..984
- (D) OTHER INFORMATION: /note= "(OCIF-DDD2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCA GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540

CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGACG CACTAAAGCA CTCAAAGACG	840
TACCACTTTC CCAAACTGT CACTCAGAGT CTAAAGAAGA CCATCAGGTT CCTTCACAGC	900
TTCACAATGT ACAAATTGTA TCAGAAGTTA TTTTATAGAA TGATAGGTAA CCAGGTCCAA	960
TCAGTAAAAA TAAGCTGCTT ATAA	984

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1200
- (D) OTHER INFORMATION: /note= "(OCIF-CL) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCAGAG GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660

AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTCAAAGA CGTACCACTT TCCCAAACT	1080
GTCACCTCAGA GTCTAAAGAA GACCATCAGG TTCCTTCACA GCTTCACAAT GTACAAATTG	1140
TATCAGAAGT TATTTTTAGA AATGATAGGT AACCAGGTCC AATCAGTAAA AATAAGCTAA	1200

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1056
- (D) OTHER INFORMATION: /note= "(OCIF-CC)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540

CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC	600
CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAAGATA TTGACCTCTG TGAAAACAGC	840
GTGCAGCGGC ACATTGGACA TGCTAACCTC ACCTTCGAGC AGCTTCGTAG CTTGATGGAA	900
AGCTTACCGG GAAAGAAAGT GGGAGCAGAA GACATTGAAA AAACAATAAA GGCATGCAAA	960
CCCAGTGACC AGATCCTGAA GCTGCTCAGT TTGTGGCGAA TAAAAAATGG CGACCAAGAC	1020
ACCTTGAAGG GCCTAATGCA CGCACTAAAG CACTGA	1056

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..819
- (D) OTHER INFORMATION: /note= "(OCIF-CDD2)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ATGAACAAC TGTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT AGATGTTACC	600

CTGTGTGAGG AGGCATTCTT CAGGTTTGCT GTTCCTACAA AGTTTACGCC TAACTGGCTT	660
AGTGTCTTGG TAGACAATTT GCCTGGCACC AAAGTAAACG CAGAGAGTGT AGAGAGGATA	720
AAACGGCAAC ACAGCTCACA AGAACAGACT TTCCAGCTGC TGAAGTTATG GAAACATCAA	780
AACAAAGACC AAGATATAGT CAAGAAGATC ATCCAATGA	819

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 594 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..594
- (D) OTHER INFORMATION: /note= "(OCIF-CDD1)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATGAACAACT TGCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC	60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC	300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA	360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCA GA GCGAAATACA	420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCCTGT	480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA	540
CACGACAACA TATGTTCCGG AAACAGTGAA TCAACTCAAA AATGTGGAAT ATGA	594

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..432
- (D) OTHER INFORMATION: /note= "(OCIF-CCR4)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```
ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC      60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG      120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC      180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT      240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC      300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA      360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA      420
GTTTGCAAAT GA                                     432
```

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..321
- (D) OTHER INFORMATION: /note= "(OCIF-CCR3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```
ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC      60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG      120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC      180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT      240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC      300
CACAACCGCG TGTGCGAATG A                                     321
```

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1182
 (D) OTHER INFORMATION: /note= "(OCIF-CBst)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCAAG	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCTTC	TCAAATGAGA	CGTCATCTAA	AGCACCCGTG	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCTTACAA	AGTTTACGCC	TAAGTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCATGCAAA	960
CCCAGTGACC	AGATCCTGAA	GCTGCTCAGT	TTGTGGCGAA	TAAAAAATGG	CGACCAAGAC	1020
ACCTTGAAGG	GCCTAATGCA	CGCACTAAAG	CACTCAAAGA	CGTACCACTT	TCCCAAAACT	1080
GTCCTCAGA	GTCTAAAGAA	GACCATCAGG	TTCCTTCACA	GCTTCACAAT	GTACAAATTG	1140
TATCAGAAGT	TATTTTTAGA	AATGATAGGT	AACCTAGTCT	AG		1182

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..966
- (D) OTHER INFORMATION: /note= "(OCIF-CSph)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

ATGAACAAC	TGCTGTGCTG	CGCGCTCGTG	TTTCTGGACA	TCTCCATTAA	GTGGACCACC	60
CAGGAAACGT	TTCCTCCAAA	GTACCTTCAT	TATGACGAAG	AAACCTCTCA	TCAGCTGTTG	120
TGTGACAAAT	GTCCTCCTGG	TACCTACCTA	AAACAACACT	GTACAGCAAA	GTGGAAGACC	180
GTGTGCGCCC	CTTGCCCTGA	CCACTACTAC	ACAGACAGCT	GGCACACCAG	TGACGAGTGT	240
CTATACTGCA	GCCCCGTGTG	CAAGGAGCTG	CAGTACGTCA	AGCAGGAGTG	CAATCGCACC	300
CACAACCGCG	TGTGCGAATG	CAAGGAAGGG	CGCTACCTTG	AGATAGAGTT	CTGCTTGAAA	360
CATAGGAGCT	GCCCTCCTGG	ATTTGGAGTG	GTGCAAGCTG	GAACCCCA	GCGAAATACA	420
GTTTGCAAAA	GATGTCCAGA	TGGGTTCCTC	TCAAATGAGA	CGTCATCTAA	AGCACCTGT	480
AGAAAACACA	CAAATTGCAG	TGTCTTTGGT	CTCCTGCTAA	CTCAGAAAGG	AAATGCAACA	540
CACGACAACA	TATGTTCCGG	AAACAGTGAA	TCAACTCAAA	AATGTGGAAT	AGATGTTACC	600
CTGTGTGAGG	AGGCATTCTT	CAGGTTTGCT	GTTCTTACAA	AGTTTACGCC	TAACTGGCTT	660
AGTGTCTTGG	TAGACAATTT	GCCTGGCACC	AAAGTAAACG	CAGAGAGTGT	AGAGAGGATA	720
AAACGGCAAC	ACAGCTCACA	AGAACAGACT	TTCCAGCTGC	TGAAGTTATG	GAAACATCAA	780
AACAAAGACC	AAGATATAGT	CAAGAAGATC	ATCCAAGATA	TTGACCTCTG	TGAAAACAGC	840
GTGCAGCGGC	ACATTGGACA	TGCTAACCTC	ACCTTCGAGC	AGCTTCGTAG	CTTGATGGAA	900
AGCTTACCGG	GAAAGAAAGT	GGGAGCAGAA	GACATTGAAA	AAACAATAAA	GGCTAGTCTA	960
GACTAG						966

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..564
- (D) OTHER INFORMATION: /note= "(OCIF-CBsp)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```
ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC      60
CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG      120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC      180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT      240
CTATACTGCA GCCCCGTGTG CAAGGAGCTG CAGTACGTCA AGCAGGAGTG CAATCGCACC      300
CACAACCGCG TGTGCGAATG CAAGGAAGGG CGCTACCTTG AGATAGAGTT CTGCTTGAAA      360
CATAGGAGCT GCCCTCCTGG ATTTGGAGTG GTGCAAGCTG GAACCCCAAG GCGAAATACA      420
GTTTGCAAAA GATGTCCAGA TGGGTTCTTC TCAAATGAGA CGTCATCTAA AGCACCCTGT      480
AGAAAACACA CAAATTGCAG TGTCTTTGGT CTCCTGCTAA CTCAGAAAGG AAATGCAACA      540
CACGACAACA TATGTTCCGG CTAG                                         564
```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..255
- (D) OTHER INFORMATION: /note= "(OCIF-Pst)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```
ATGAACAAC T GCTGTGCTG CGCGCTCGTG TTTCTGGACA TCTCCATTAA GTGGACCACC      60
```

CAGGAAACGT TTCCTCCAAA GTACCTTCAT TATGACGAAG AAACCTCTCA TCAGCTGTTG	120
TGTGACAAAT GTCCTCCTGG TACCTACCTA AAACAACACT GTACAGCAAA GTGGAAGACC	180
GTGTGCGCCC CTTGCCCTGA CCACTACTAC ACAGACAGCT GGCACACCAG TGACGAGTGT	240
CTATACCTAG TCTAG	255

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1317
- (D) OTHER INFORMATION: /note= "human OCIF genomic DNA-1"

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1173..1202
- (D) OTHER INFORMATION: /note= "amino acid residues -21 to -12"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CTGGAGACAT ATAACTTGAA CACTTGGCCC TGATGGGGAA GCAGCTCTGC AGGGACTTTT	60
TCAGCCATCT GTAAACAATT TCAGTGGCAA CCCGCGAACT GTAATCCATG AATGGGACCA	120
CACTTTACAA GTCATCAAGT CTAAGTTCTA GACCAGGGAA TTAATGGGGG AGACAGCGAA	180
CCCTAGAGCA AAGTGCCAAA CTTCTGTCTA TAGCTTGAGG CTAGTGGAAA GACCTCGAGG	240
AGGCTACTCC AGAAGTTCAG CGCGTAGGAA GCTCCGATAC CAATAGCCCT TTGATGATGG	300
TGGGGTTGGT GAAGGGAACA GTGCTCCGCA AGGTTATCCC TGCCCCAGGC AGTCCAATTT	360
TCACTCTGCA GATTCTCTCT GGCTCTAACT ACCCCAGATA ACAAGGAGTG AATGCAGAAT	420
AGCACGGGCT TTAGGGCCAA TCAGACATTA GTTAGAAAAA TTCCTACTAC ATGGTTTATG	480
TAAACTTGAA GATGAATGAT TGCGAATCC CCGAAAAGGG CTCAGACAAT GCCATGCATA	540
AAGAGGGGCC CTGTAATTTG AGGTTTCAGA ACCCGAAGTG AAGGGGTCAG GCAGCCGGGT	600
ACGGCGGAAA CTCACAGCTT TCGCCCAGCG AGAGGACAAA GGTCTGGGAC AACTCCAAC	660
TGCGTCCGGA TCTTGGCTGG ATCGGACTCT CAGGGTGGAG GAGACACAAG CACAGCAGCT	720
GCCCAGCGTG TGCCCAGCCC TCCCACCGCT GGTCCCGGCT GCCAGGAGGC TGGCCGCTGG	780

CGGGAAGGGG CCGGGAACC TCAGAGCCCC GCGGAGACAG CAGCCGCCTT GTTCCTCAGC	840
CCGGTGGCTT TTTTTCCTCC TGCTCTCCCA GGGGACAGAC ACCACCGCCC CACCCCTCAC	900
GCCCCACCTC CCTGGGGGAT CCTTTCGCC CCAGCCCTGA AAGCGTTAAT CCTGGAGCTT	960
TCTGCACACC CCCCAGCCGC TCCCGCCCAA GCTTCCTAAA AAAGAAAGGT GCAAAGTTTG	1020
GTCCAGGATA GAAAAATGAC TGATCAAAGG CAGGCGATAC TTCCTGTTGC CGGGACGCTA	1080
TATATAACGT GATGAGCGCA CGGGCTGCGG AGACGCACCG GAGCGCTCGC CCAGCCGCCG	1140
CCTCCAAGCC CCTGAGGTTT CCGGGGACCA CAATGAACAA GTTGCTGTGC TGC GCGCTCG	1200
TGGTAAGTCC CTGGGCCAGC CGACGGGTGC CCGGCGCCTG GGGAGGCTGC TGCCACCTGG	1260
TCTCCAACC TCCCAGCGGA CCGGCGGGGA AAAAGGCTCC ACTCGCTCCC TCCAAG	1317

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 130..162
- (D) OTHER INFORMATION: /note= "amino acid residues -11 to -1"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(130..162, 163..498, 4503..4694, 6715..6939, 8960..9346)

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: join(163..498, 4503..4694, 6715..6939, 8960..9346)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCTTACTTTG TGCCAAATCT CATTAGGCTT AAGGTAATAC AGGACTTTGA GTCAAATGAT	60
ACTGTTGCAC ATAAGAACAA ACCTATTTTC ATGCTAAGAT GATGCCACTG TGTTCCTTTC	120
TCCTTCTAG TTT CTG GAC ATC TCC ATT AAG TGG ACC ACC CAG GAA ACG	168
Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr	
-11 -10 -5 1	
TTT CCT CCA AAG TAC CTT CAT TAT GAC GAA GAA ACC TCT CAT CAG CTG	216
Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu	

5	10	15	
TTG TGT GAC AAA TGT CCT CCT GGT ACC TAC CTA AAA CAA CAC TGT ACA			264
Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr			
20	25	30	
GCA AAG TGG AAG ACC GTG TGC GCC CCT TGC CCT GAC CAC TAC TAC ACA			312
Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr			
35	40	45	50
GAC AGC TGG CAC ACC AGT GAC GAG TGT CTA TAC TGC AGC CCC GTG TGC			360
Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys			
55	60	65	
AAG GAG CTG CAG TAC GTC AAG CAG GAG TGC AAT CGC ACC CAC AAC CGC			408
Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg			
70	75	80	
GTG TGC GAA TGC AAG GAA GGG CGC TAC CTT GAG ATA GAG TTC TGC TTG			456
Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu			
85	90	95	
AAA CAT AGG AGC TGC CCT CCT GGA TTT GGA GTG GTG CAA GCT			498
Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala			
100	105	110	
GGTACGTGTC AATGTGCAGC AAAATTAATT AGGATCATGC AAAGTCAGAT AGTTGTGACA			558
GTTTAGGAGA ACACTTTTGT TCTGATGACA TTATAGGATA GCAAATTGCA AAGGTAATGA			618
AACCTGCCAG GTAGGTACTA TGTGTCTGGA GTGCTTCCAA AGGACCATTG CTCAGAGGAA			678
TACTTTGCCA CTACAGGGCA ATTTAATGAC AAATCTCAAA TGCAGCAAAT TATTCTCTCA			738
TGAGATGCAT GATGGTTTTT TTTTTTTTTT TTAAAGAAAC AAACCTCAAGT TGCACATTG			798
ATAGTTGATC TATACCTCTA TATTTCACTT CAGCATGGAC ACCTTCAAAC TGCAGCACTT			858
TTTGACAAAC ATCAGAAATG TTAATTTATA CCAAGAGAGT AATTATGCTC ATATTAATGA			918
GA CTCTGGAG TGCTAACAAT AAGCAGTTAT AATTAATTAT GTAAAAAATG AGAATGGTGA			978
GGGGAATTGC ATTTCAATTAT TAAAAACAAG GCTAGTTCTT CCTTTAGCAT GGGAGCTGAG			1038
TGTTTGAGGAG GGTAAGGACT ATAGCAGAAT CTCTTCAATG AGCTTATTCT TTATCTTAGA			1098
CAAAACAGAT TGTCAAGCCA AGAGCAAGCA CTGCGCTATA AACCAAGTGC TTTCTCTTTT			1158
GCATTTTGAA CAGCATTGGT CAGGGCTCAT GTGTATTGAA TCTTTTAAAC CAGTAACCCA			1218
CGTTTTTTTT CTGCCACATT TGCGAAGCTT CAGTGCAGCC TATAACTTTT CATAGCTTGA			1278
GAAAATTAAG AGTATCCACT TACTTAGATG GAAGAAGTAA TCAGTATAGA TTCTGATGAC			1338
TCAGTTTGAA GCAGTGTTC TCAACTGAAG CCCTGCTGAT ATTTTAAGAA ATATCTGGAT			1398
TCCTAGGCTG GACTCCTTTT TGTGGGCAGC TGTCTGCGC ATTGTAGAAT TTTGGCAGCA			1458

CCCCTGGACT	CTAGCCACTA	GATACCAATA	GCAGTCCTTC	CCCCATGTGA	CAGCCAAAAA	1518
TGTCTTCAGA	CACTGTCAAA	TGTCGCCAGG	TGGCAAAATC	ACTCCTGGTT	GAGAACAGGG	1578
TCATCAATGC	TAAGTATCTG	TAACTATTTT	AACTCTCAAA	ACTTGTGATA	TACAAAGTCT	1638
AAATTATTAG	ACGACCAATA	CTTTAGGTTT	AAAGGCATAC	AAATGAAACA	TTCAAAAATC	1698
AAAATCTATT	CTGTTTCTCA	AATAGTGAAT	CTTATAAAAT	TAATCACAGA	AGATGCAAAT	1758
TGCATCAGAG	TCCCTTAAAA	TTCCTCTTCG	TATGAGTATT	TGAGGGAGGA	ATTGGTGATA	1818
GTTCTACTT	TCTATTGGAT	GGTACTTTGA	GACTCAAAAG	CTAAGCTAAG	TTGTGTGTGT	1878
GTCAGGGTGC	GGGGTGTGGA	ATCCCATCAG	ATAAAAGCAA	ATCCATGTAA	TTCATTCACT	1938
AAGTTGTATA	TGTAGAAAAA	TGAAAAGTGG	GCTATGCAGC	TTGGAAACTA	GAGAATTTTG	1998
AAAAATAATG	GAAATCACAA	GGATCTTTCT	TAAATAAGTA	AGAAAATCTG	TTTGTAGAAT	2058
GAAGCAAGCA	GGCAGCCAGA	AGACTCAGAA	CAAAAGTACA	CATTTTACTC	TGTGTACACT	2118
GGCAGCACAG	TGGGATTTAT	TTACCTCTCC	CTCCCTAAAA	ACCCACACAG	CGGTTCTCT	2178
TGGGAAATAA	GAGGTTTCCA	GCCCAAAGAG	AAGGAAAGAC	TATGTGGTGT	TACTCTAAAA	2238
AGTATTTAAT	AACCGTTTTG	TTGTTGCTGT	TGCTGTTTTG	AAATCAGATT	GTCTCCTCTC	2298
CATATTTTAT	TTACTTCATT	CTGTTAATTC	CTGTGGAATT	ACTTAGAGCA	AGCATGGTGA	2358
ATTCTCAACT	GTAAAGCCAA	ATTTCTCCAT	CATTATAATT	TCACATTTTG	CCTGGCAGGT	2418
TATAATTTTT	ATATTTCCAC	TGATAGTAAT	AAGGTAAAAT	CATTACTTAG	ATGGATAGAT	2478
CTTTTTCATA	AAAAGTACCA	TCAGTTATAG	AGGGAAGTCA	TGTTCATGTT	CAGGAAGGTC	2538
ATTAGATAAA	GCTTCTGAAT	ATATTATGAA	ACATTAGTTC	TGTCATTCTT	AGATTCTTTT	2598
TGTTAAATAA	CTTTAAAAGC	TAACTTACCT	AAAAGAAATA	TCTGACACAT	ATGAACTTCT	2658
CATTAGGATG	CAGGAGAAGA	CCCAAGCCAC	AGATATGTAT	CTGAAGAATG	AACAAGATTC	2718
TTAGGCCCGG	CACGGTGGCT	CACATCTGTA	ATCTCAAGAG	TTTGAGAGGT	CAAGGCGGGC	2778
AGATCACCTG	AGGTCAGGAG	TTCAAGACCA	GCCTGGCCAA	CATGATGAAA	CCCTGCCTCT	2838
ACTAAAAATA	CAAAAATTAG	CAGGGCATGG	TGGTGCATGC	CTGCAACCCT	AGCTACTCAG	2898
GAGGCTGAGA	CAGGAGAATC	TCTTGAACCC	TCGAGGCGGA	GGTTGTGGTG	AGCTGAGATC	2958
CCTCTACTGC	ACTCCAGCCT	GGGTGACAGA	GATGAGACTC	CGTCCCTGCC	GCCGCCCCCG	3018
CCTTCCCCCC	CAAAAAGATT	CTTCTTCATG	CAGAACATAC	GGCAGTCAAC	AAAGGGAGAC	3078
CTGGGTCCAG	GTGTCCAAGT	CACTTATTTT	GAGTAAATTA	GCAATGAAAG	AATGCCATGG	3138

AATCCCTGCC CAAATACCTC TGCTTATGAT ATTGTAGAAT TTGATATAGA GTTGTATCCC	3198
ATTTAAGGAG TAGGATGTAG TAGGAAAGTA CTAAAAACAA ACACACAAAC AGAAAACCCT	3258
CTTTGCTTTG TAAGGTGGTT CCTAAGATAA TGTCAGTGCA ATGCTGGAAA TAATATTTAA	3318
TATGTGAAGG TTTTAGGCTG TGTTTTCCCC TCCTGTTCTT TTTTCTGCC AGCCCTTTGT	3378
CATTTTTGCA GGTCAATGAA TCATGTAGAA AGAGACAGGA GATGAAACTA GAACCAGTCC	3438
ATTTTGCCCC TTTTTTTATT TTCTGGTTTT GGTAAGAT ACAATGAGGT AGGAGGTTGA	3498
GATTTATAAA TGAAGTTTAA TAAGTTTCTG TAGCTTTGAT TTTTCTCTTT CATATTTGTT	3558
ATCTTGCATA AGCCAGAATT GGCCTGTAAA ATCTACATAT GGATATTGAA GTCTAAATCT	3618
GTTCAACTAG CTTACACTAG ATGGAGATAT TTTCATATTC AGATACACTG GAATGTATGA	3678
TCTAGCCATG CGTAATATAG TCAAGTGTTT GAAGGTATTT ATTTTAAATA GCGTCTTTAG	3738
TTGTGGACTG GTTCAAGTTT TTCTGCCAAT GATTTCTTCA AATTTATCAA ATATTTTCC	3798
ATCATGAAGT AAAATGCCCT TGCAGTCACC CTTCTGAAG TTTGAACGAC TCTGCTGTTT	3858
TAAACAGTTT AAGCAAATGG TATATCATCT TCCGTTTACT ATGTAGCTTA ACTGCAGGCT	3918
TACGCTTTTG AGTCAGCGGC CAACTTTATT GCCACCTTCA AAAGTTTATT ATAATGTTGT	3978
AAATTTTAC TTCTCAAGGT TAGCATACTT AGGAGTTGCT TCACAATTAG GATTCAGGAA	4038
AGAAAGAACT TCAGTAGGAA CTGATTGGAA TTTAATGATG CAGCATTCAA TGGGTACTAA	4098
TTTCAAAGAA TGATATTACA GCAGACACAC AGCAGTTATC TTGATTTTCT AGGAATAATT	4158
GTATGAAGAA TATGGCTGAC AACACGGCCT TACTGCCACT CAGCGGAGGC TGGACTAATG	4218
AACACCCTAC CCTTCTTTCC TTTCTCTCA CATTTTCATGA GCGTTTTGTA GGTAACGAGA	4278
AAATTGACTT GCATTTGCAT TACAAGGAGG AGAACTGGC AAAGGGGATG ATGGTGGAAG	4338
TTTTGTTCTG TCTAATGAAG TGAAAAATGA AAATGCTAGA GTTTTGTGCA ACATAATAGT	4398
AGCAGTAAAA ACCAAGTGAA AAGTCTTTCC AAAACTGTGT TAAGAGGGCA TCTGCTGGGA	4458
AACGATTTGA GGAGAAGGTA CTAAATTGCT TGGTATTTTC CGTA GGA ACC CCA GAG	4514
	Gly Thr Pro Glu
	115
CGA AAT ACA GTT TGC AAA AGA TGT CCA GAT GGG TTC TTC TCA AAT GAG	4562
Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn Glu	
120 125 130	
ACG TCA TCT AAA GCA CCC TGT AGA AAA CAC ACA AAT TGC AGT GTC TTT	4610
Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser Val Phe	
135 140 145	
GGT CTC CTG CTA ACT CAG AAA GGA AAT GCA ACA CAC GAC AAC ATA TGT	4658

[illegible]

TCCTATGTAA TGTCTACTTA TATATCTGTA TCTATCTCTT GCTTTGTTTC CAAAGGTAAA	6264
CTATGTGTCT AAATGTGGGC AAAAAATAAC ACACTATTCC AAATTACTGT TCAAATTCCT	6324
TTAAGTCAGT GATAATTATT TGTTTTGACA TTAATCATGA AGTTCCTGT GGGTACTAGG	6384
TAAACCTTTA ATAGAATGTT AATGTTTGTA TTCATTATAA GAATTTTTGG CTGTTACTTA	6444
TTTACAACAA TATTTCACTC TAATTAGACA TTTACTAAAC TTTCTCTTGA AAACAATGCC	6504
CAAAAAAGAA CATTAGAAGA CACGTAAGCT CAGTTGGTCT CTGCCACTAA GACCAGCCAA	6564
CAGAAGCTTG ATTTTATTCA AACTTTGCAT TTTAGCATAT TTTATCTTGG AAAATTCAAT	6624
TGTGTTGGTT TTTTGTTTTT GTTTGTATTG AATAGACTCT CAGAAATCCA ATTGTTGAGT	6684
AAATCTTCTG GGTTTTCTAA CCTTTCTTTA GAT GTT ACC CTG TGT GAG GAG GCA	6738
Asp Val Thr Leu Cys Glu Glu Ala	180
TTC TTC AGG TTT GCT GTT CCT ACA AAG TTT ACG CCT AAC TGG CTT AGT	6786
Phe Phe Arg Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser	
185 190 195 200	
GTC TTG GTA GAC AAT TTG CCT GGC ACC AAA GTA AAC GCA GAG AGT GTA	6834
Val Leu Val Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val	
205 210 215	
GAG AGG ATA AAA CGG CAA CAC AGC TCA CAA GAA CAG ACT TTC CAG CTG	6882
Glu Arg Ile Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu	
220 225 230	
CTG AAG TTA TGG AAA CAT CAA AAC AAA GAC CAA GAT ATA GTC AAG AAG	6930
Leu Lys Leu Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys	
235 240 245	
ATC ATC CAA GGTAATTACA TTCCAAAATA CGTCTTTGTA CGATTTTGTA	6979
Ile Ile Gln	250
GTATCATCTC TCTCTCTGAG TTGAACACAA GGCCTCCAGC CACATTCTTG GTCAAACCTTA	7039
CATTTTCCCT TTCTTGAATC TTAACCAGCT AAGGCTACTC TCGATGCATT ACTGCTAAAG	7099
CTACCACTCA GAATCTCTCA AAAACTCATC TTCTCACAGA TAACACCTCA AAGCTTGATT	7159
TTCTCTCCTT TCACACTGAA ATCAAATCTT GCCCATAGGC AAAGGGCAGT GTCAAGTTTG	7219
CCACTGAGAT GAAATTAGGA GAGTCCAAAC TGTAGAATTC ACGTTGTGTG TTATTACTTT	7279
CACGAATGTC TGTATTATTA ACTAAAGTAT ATATTGGCAA CTAAGAAGCA AAGTGATATA	7339
AACATGATGA CAAATTAGGC CAGGCATGGT GGCTTACTCC TATAATCCCA ACATTTTGGG	7399
GGGCCAAGGT AGGCAGATCA CTTGAGGTCA GGATTTC AAG ACCAGCCTGA CCAACATGGT	7459
GAAACCTTGT CTCTACTAAA AATACAAAAA TTAGCTGGGC ATGGTAGCAG GCACTTCTAG	7519

TACCAGCTAC	TCAGGGCTGA	GGCAGGAGAA	TCGCTTGAAC	CCAGGAGATG	GAGGTTGCAG	7579
TGAGCTGAGA	TTGTACCACT	GCACTCCAGT	CTGGGCAACA	GAGCAAGATT	TCATCACACA	7639
CACACACACA	CACACACACA	CACACATTAG	AAATGTGTAC	TTGGCTTTGT	TACCTATGGT	7699
ATTAGTGCAT	CTATTGCATG	GAACTTCCAA	GCTACTCTGG	TTGTGTTAAG	CTCTTCATTG	7759
GGTACAGGTC	ACTAGTATTA	AGTTCAGGTT	ATTCGGATGC	ATTCCACGGT	AGTGATGACA	7819
ATTCATCAGG	CTAGTGTGTG	TGTTACCTT	GTCACTCCCA	CCACTAGACT	AATCTCAGAC	7879
CTTCACTCAA	AGACACATTA	CACTAAAGAT	GATTTGCTTT	TTTGTGTTTA	ATCAAGCAAT	7939
GGTATAAACC	AGCTTGACTC	TCCCCAAACA	GTTTTTCGTA	CTACAAAGAA	GTTTATGAAG	7999
CAGAGAAATG	TGAATTGATA	TATATATGAG	ATTCTAACCC	AGTTCAGCA	TTGTTTCATT	8059
GTGTAATTGA	AATCATAGAC	AAGCCATTTT	AGCCTTTGCT	TTCTTATCTA	AAAAAAAAAA	8119
AAAAAAAAATG	AAGGAAGGGG	TATTAAAAGG	AGTGATCAAA	TTTAAACATT	CTCTTTAATT	8179
AATTCATTTT	TAATTTTACT	TTTTTTCATT	TATTGTGCAC	TTACTATGTG	GTACTGTGCT	8239
ATAGAGGCTT	TAACATTTAT	AAAAACACTG	TGAAAGTTGC	TTCAGATGAA	TATAGGTAGT	8299
AGAACGGCAG	AACTAGTATT	CAAAGCCAGG	TCTGATGAAT	CCAAAAACAA	ACACCCATTA	8359
CTCCCATTTT	CTGGGACATA	CTTACTCTAC	CCAGATGCTC	TGGGCTTTGT	AATGCCTATG	8419
TAAATAACAT	AGTTTTATGT	TTGGTTATTT	TCCTATGTAA	TGTCTACTTA	TATATCTGTA	8479
TCTATCTCTT	GCTTTGTTTC	CAAAGGTAAA	CTATGTGTCT	AAATGTGGGC	AAAAAATAAC	8539
ACACTATTCC	AAATTACTGT	TCAAATTCCT	TTAAGTCAGT	GATAATTATT	TGTTTTGACA	8599
TTAATCATGA	AGTTCCTGT	GGGTACTAGG	TAAACCTTTA	ATAGAATGTT	AATGTTTGTA	8659
TTCATTATAA	GAATTTTTGG	CTGTTACTTA	TTTACAACAA	TATTTCACTC	TAATTAGACA	8719
TTTACTAAAC	TTTCTCTTGA	AAACAATGCC	CAAAAAAGAA	CATTAGAAGA	CACGTAAGCT	8779
CAGTTGGTCT	CTGCCACTAA	GACCAGCCAA	CAGAAGCTTG	ATTTTATTCA	AACTTTGCAT	8839
TTTAGCATAT	TTTATCTTGG	AAAATTCAAT	TGTGTTGGTT	TTTTGTTTTT	GTTTGTATTG	8899
AATAGACTCT	CAGAAATCCA	ATTGTTGAGT	AAATCTTCTG	GGTTTTCTAA	CCTTTCTTTA	8959
GAT ATT GAC CTC TGT GAA AAC AGC GTG CAG CGG CAC ATT GGA CAT GCT						9007
Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala						
255			260		265	
AAC CTC ACC TTC GAG CAG CTT CGT AGC TTG ATG GAA AGC TTA CCG GGA						9055
Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly						
270			275		280	

AAG AAA GTG GGA GCA GAA GAC ATT GAA AAA ACA ATA AAG GCA TGC AAA Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys 285 290 295	9103
CCC AGT GAC CAG ATC CTG AAG CTG CTC AGT TTG TGG CGA ATA AAA AAT Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn 300 305 310 315	9151
GGC GAC CAA GAC ACC TTG AAG GGC CTA ATG CAC GCA CTA AAG CAC TCA Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser 320 325 330	9199
AAG ACG TAC CAC TTT CCC AAA ACT GTC ACT CAG AGT CTA AAG AAG ACC Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr 335 340 345	9247
ATC AGG TTC CTT CAC AGC TTC ACA ATG TAC AAA TTG TAT CAG AAG TTA Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu 350 355 360	9295
TTT TTA GAA ATG ATA GGT AAC CAG GTC CAA TCA GTA AAA ATA AGC TGC Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys 365 370 375	9343
TTA TAACTGGAAA TGGCCATTGA GCTGTTTCCT CACAATTGGC GAGATCCCAT Leu 380	9396
GGATGAGTAA ACTGTTTCTC AGGCACTTGA GGCTTTCAGT GATATCTTTC TCATTACCAG	9456
TGACTAATTT TGCCACAGGG TACTAAAAGA AACTATGATG TGGAGAAAGG ACTAACATCT	9516
CCTCCAATAA ACCCCAAATG GTTAATCCAA CTGTCAGATC TGGATCGTTA TCTACTGACT	9576
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CTCCACTGGG CCTTACTAAA TATGGGAATG TCTAACTTAA ATAGCTTTGG GATTCCAGCT	9696
ATGCTAGAGG CTTTTATTAG AAAGCCATAT TTTTTTCTGT AAAAGTTACT AATATATCTG	9756
TAACACTATT ACAGTATTGC TATTTATATT CATTCAGATA TAAGATTTGG ACATATTATC	9816
ATCCTATAAA GAAACGGTAT GACTTAATTT TAGAAAGAAA ATTATATTCT GTTTATTATG	9876
ACAAATGAAA GAGAAAATAT ATATTTTAA TGGAAAGTTT GTAGCATTTT TCTAATAGGT	9936
ACTGCCATAT TTTTCTGTGT GGAGTATTTT TATAATTTTA TCTGTATAAG CTGTAATATC	9996
ATTTTATAGA AAATGCATTA TTTAGTCAAT TGTTTAATGT TGGAAAACAT ATGAAATATA	10056
AATTATCTGA ATATTAGATG CTCTGAGAAA TTGAATGTAC CTTATTTAAA AGATTTTATG	10116
GTTTTATAAC TATATAAATG ACATTATTAA AGTTTTCAAA TTATTTTTTA TTGCTTTCTC	10176
TGTTGCTTTT ATTT	10190

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Phe	Leu	Asp	Ile	Ser	Ile	Lys	Trp	Thr	Thr	Gln	Glu	Thr	Phe	Pro	Pro	
-11	-10					-5					1				5	
Lys	Tyr	Leu	His	Tyr	Asp	Glu	Glu	Thr	Ser	His	Gln	Leu	Leu	Cys	Asp	
				10					15					20		
Lys	Cys	Pro	Pro	Gly	Thr	Tyr	Leu	Lys	Gln	His	Cys	Thr	Ala	Lys	Trp	
			25					30					35			
Lys	Thr	Val	Cys	Ala	Pro	Cys	Pro	Asp	His	Tyr	Tyr	Thr	Asp	Ser	Trp	
		40					45					50				
His	Thr	Ser	Asp	Glu	Cys	Leu	Tyr	Cys	Ser	Pro	Val	Cys	Lys	Glu	Leu	
	55					60					65					
Gln	Tyr	Val	Lys	Gln	Glu	Cys	Asn	Arg	Thr	His	Asn	Arg	Val	Cys	Glu	
70					75					80					85	
Cys	Lys	Glu	Gly	Arg	Tyr	Leu	Glu	Ile	Glu	Phe	Cys	Leu	Lys	His	Arg	
				90					95					100		
Ser	Cys	Pro	Pro	Gly	Phe	Gly	Val	Val	Gln	Ala	Gly	Thr	Pro	Glu	Arg	
			105					110					115			
Asn	Thr	Val	Cys	Lys	Arg	Cys	Pro	Asp	Gly	Phe	Phe	Ser	Asn	Glu	Thr	
		120					125					130				
Ser	Ser	Lys	Ala	Pro	Cys	Arg	Lys	His	Thr	Asn	Cys	Ser	Val	Phe	Gly	
	135					140					145					
Leu	Leu	Leu	Thr	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Ile	Cys	Ser	
150					155					160					165	
Gly	Asn	Ser	Glu	Ser	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	Leu	Cys	
				170					175					180		
Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Phe	Thr	Pro	Asn	
			185					190					195			
Trp	Leu	Ser	Val	Leu	Val	Asp	Asn	Leu	Pro	Gly	Thr	Lys	Val	Asn	Ala	
		200					205						210			
Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Gln	His	Ser	Ser	Gln	Glu	Gln	Thr	
	215					220					225					
Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	Lys	Asp	Gln	Asp	Ile	

230		235		240		245									
Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	Asn	Ser	Val	Gln
			250						255					260	
Arg	His	Ile	Gly	His	Ala	Asn	Leu	Thr	Phe	Glu	Gln	Leu	Arg	Ser	Leu
		265						270					275		
Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Val	Gly	Ala	Glu	Asp	Ile	Glu	Lys
		280					285					290			
Thr	Ile	Lys	Ala	Cys	Lys	Pro	Ser	Asp	Gln	Ile	Leu	Lys	Leu	Leu	Ser
	295					300					305				
Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	Leu	Met
310					315					320					325
His	Ala	Leu	Lys	His	Ser	Lys	Thr	Tyr	His	Phe	Pro	Lys	Thr	Val	Thr
			330						335					340	
Gln	Ser	Leu	Lys	Lys	Thr	Ile	Arg	Phe	Leu	His	Ser	Phe	Thr	Met	Tyr
		345						350					355		
Lys	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	Val	Gln
	360						365					370			
Ser	Val	Lys	Ile	Ser	Cys	Leu									
	375					380									

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "synthetic DNA (primer 2F)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CARGARCARA CNTTYCARYT

20

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..21

(D) OTHER INFORMATION: /note= "synthetic DNA (primer 3R)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

YTTTACATN GTRAANSWRT G

21